

10615383.txt
Title: US- 10- 615- 383A- 7_COPY_252_1895
Perfect score: 1644
Sequence: 1 gagaat acagt acaagacgt act t gcct cct gaaaaaact 1644

RESULT 3

ABN93014

ID ABN93014 standard; DNA; 2793 BP.

XX

AC ABN93014;

XX

DT 24- JUL- 2002 (first entry)

XX

DE Staphyl ococcus epi der mi di s ORF nucl ei c aci d sequence SEQ ID NO: 2477.

XX

KW Staphyl ococcus epi der mi di s; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy; gene; ds.

XX

OS Staphyl ococcus epi der mi di s.

XX

PN US6380370- B1.

XX

PD 30- APR- 2002.

XX

PF 13- AUG- 1998; 98US- 00134001.

XX

PR 14- AUG- 1997; 97US- 0055779P.

PR

08- NOV- 1997; 97US- 0064964P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Doucet t e- St amm LA, Bush D;

XX

DR WPI ; 2002- 381255/ 41.

DR

P- PSDB; ABP40469.

XX

PT Novel isolated nucleic acid encoding a Staphyl ococcus epi der mi s
PT polypeptide, useful for diagnosing and treating bacterial infections.

XX

PS Disclosure; SEQ ID NO 2477; 267pp; English.

XX

CC ABN90538 to ABN93374 represent Staphyl ococcus epi der mi di s open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epi der mi di s sequences have
CC antibacterial activity and can be used in gene therapy. The sequences can
CC also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epi der mi di s infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epi der mi di s life cycle
CC or inhibit S. epi der mi di s infection. N.B. The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site

XX

SQ Sequence 2793 BP; 1149 A; 423 C; 497 G; 724 T; 0 U; 0 Other;

Query Match 100.0% Score 1644; DB 1; Length 2793;

Best Local Similarity 100.0%

Matches 1644; Conservative 0; M smatches 0; Indels 0; Gaps 0;

Qy 1 GAGAATACAGTACAAGACGTTAAAGATTGAATATGGATGATGAATTATCAGATAGCAAT 60
Db 151 GAGAATACAGTACAAGACGTTAAAGATTGAATATGGATGATGAATTATCAGATAGCAAT 210

Qy 61 GATCAGTCCAGTAATGAAGAAAAGAATGATGTAATCAATAATAGTCAGTCAATAAACACC 120
 Db 211 GATCAGTCCAGTAATGAAGAAAAGAATGATGTAATCAATAATAGTCAGTCAATAAACACC 270
 Qy 121 GATGATGATAACCAAATAAAAAAGAAGAAACGAATAGCAACGATGCCATAGAAAATCGC 180
 Db 271 GATGATGATAACCAAATAAAAAAGAAGAAACGAATAGCAACGATGCCATAGAAAATCGC 330
 Qy 181 TCTAAAGATATAACACAGTCAACAACAAATGTAGATGAAAAOGAAGCAACATTTTTACAA 240
 Db 331 TCTAAAGATATAACACAGTCAACAACAAATGTAGATGAAAAOGAAGCAACATTTTTACAA 390
 Qy 241 AAGACCCCTCAAGATAATACTCAGCTTAAAGAAGAAGTGGTAAAAGAACCCCTCATCAGTC 300
 Db 391 AAGACCCCTCAAGATAATACTCAGCTTAAAGAAGAAGTGGTAAAAGAACCCCTCATCAGTC 450
 Qy 301 GAATCCTCAAATTCATCAATGGATACTGOCACAAACCATCTCATACAACAATAAATAGT 360
 Db 451 GAATCCTCAAATTCATCAATGGATACTGOCACAAACCATCTCATACAACAATAAATAGT 510
 Qy 361 GAAGCATCTATTCAAACAAGTGATAATGAAGAAAATTCCCGGTATCAGATTTTGCTAAC 420
 Db 511 GAAGCATCTATTCAAACAAGTGATAATGAAGAAAATTCCCGGTATCAGATTTTGCTAAC 570
 Qy 421 TCTAAAATAATAGAGAGTAACACTGAATCCAATAAAGAAGAGAATACTATAGAGCAACCT 480
 Db 571 TCTAAAATAATAGAGAGTAACACTGAATCCAATAAAGAAGAGAATACTATAGAGCAACCT 630
 Qy 481 AACAAAGTAAGAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAATATAGATGAA 540
 Db 631 AACAAAGTAAGAGAAGATTCAATAACAAGTCAACCGTCTAGCTATAAAAATATAGATGAA 690
 Qy 541 AAAATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAATAAGGTT 600
 Db 691 AAAATTTCAAATCAAGATGAGTTATTAAATTTACCAATAAATGAATATGAAAATAAGGTT 750
 Qy 601 AGACCGTTATCTACAACATCTGOCACAAACCATGAGTAAGCGTGTAAACGTAAATCAATTA 660
 Db 751 AGACCGTTATCTACAACATCTGOCACAAACCATGAGTAAGCGTGTAAACGTAAATCAATTA 810
 Qy 661 GCGGCAGAACAAAGGTTGAATGTTAATCATTTAATTAAAGTTACTGATCAAAGTATTACT 720
 Db 811 GCGGCAGAACAAAGGTTGAATGTTAATCATTTAATTAAAGTTACTGATCAAAGTATTACT 870
 Qy 721 GAAGGATATGATGATAGTGATGGTATTATTAAAGCACATGATGCTGAAAACCTTAATCTAT 780
 Db 871 GAAGGATATGATGATAGTGATGGTATTATTAAAGCACATGATGCTGAAAACCTTAATCTAT 930
 Qy 781 GATGTAACTTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGAATATA 840
 Db 931 GATGTAACTTTTGAAGTAGATGATAAGGTGAAATCTGGTGATACGATGACAGTGAATATA 990
 Qy 841 GATAAGAATACAGTTCCATCAGATTTAACCGATAGTTTTGCAATACCAAAAAATAAAGAT 900
 Db 991 GATAAGAATACAGTTCCATCAGATTTAACCGATAGTTTTGCAATACCAAAAAATAAAGAT 1050
 Qy 901 AATTCTGGAGAAATCATCGCTACAGGTACTTATGACAACACAAATAAACAAATTACCTAC 960
 Db 1051 AATTCTGGAGAAATCATCGCTACAGGTACTTATGACAACACAAATAAACAAATTACCTAC 1110
 Qy 961 ACTTTTACAGATTATGTAGATAAATATGAAAATATTAAAGCGCACCTTAAATTAACATCA 1020
 Db 1111 ACTTTTACAGATTATGTAGATAAATATGAAAATATTAAAGCGCACCTTAAATTAACATCA 1170

```

Qy      1021 TACATTGATAAATCAAAGGTTCCAAATAATAAACTAAGTTAGATGTAGAATATAAGACG 1080
Db      1171 TACATTGATAAATCAAAGGTTCCAAATAATAAACTAAGTTAGATGTAGAATATAAGACG 1230
Qy      1081 GCOCTTTTCATCAGTAAATAAAACAATTACGGTTGAATATCAAAAAOCTAACGAAAATCGG 1140
Db      1231 GCOCTTTTCATCAGTAAATAAAACAATTACGGTTGAATATCAAAAAOCTAACGAAAATCGG 1290
Qy      1141 ACTGCTAAOCTTCAAAGTATGTTACAAACATAGATACGAAAAAOCATACAGTTGAGCAA 1200
Db      1291 ACTGCTAAOCTTCAAAGTATGTTACAAACATAGATACGAAAAAOCATACAGTTGAGCAA 1350
Qy      1201 ACGATTTATATTAAOCTCTTGGTTATTGAGCAAAGAAACAAATGTAATATTTGAGGG 1260
Db      1351 ACGATTTATATTAAOCTCTTGGTTATTGAGCAAAGAAACAAATGTAATATTTGAGGG 1410
Qy      1261 AATGGOGATGAAGGTTCAACAATTATOGAOGATAGTACAATCATTAAAGTTTATAAGGTT 1320
Db      1411 AATGGOGATGAAGGTTCAACAATTATOGAOGATAGTACAATCATTAAAGTTTATAAGGTT 1470
Qy      1321 GGAGATAATCAAAATTTACCAGATAGTAACAGAATTTATGATTACAGTGAATATGAAGAT 1380
Db      1471 GGAGATAATCAAAATTTACCAGATAGTAACAGAATTTATGATTACAGTGAATATGAAGAT 1530
Qy      1381 GTCACAAATGATGATTATGOCCAATTAGGAAATAATAATGACGTGAATATTAATTTTGGT 1440
Db      1531 GTCACAAATGATGATTATGOCCAATTAGGAAATAATAATGACGTGAATATTAATTTTGGT 1590
Qy      1441 AATATAGATTCACCATATATTATTAAAGTTATTAGTAAATATGAOCTAATAAGGACGAT 1500
Db      1591 AATATAGATTCACCATATATTATTAAAGTTATTAGTAAATATGAOCTAATAAGGACGAT 1650
Qy      1501 TACACGACGATACAGCAAACGTGACAATGCAAAOAGCTATAAATGAGTATACTGGTGAG 1560
Db      1651 TACACGACGATACAGCAAACGTGACAATGCAAAOAGCTATAAATGAGTATACTGGTGAG 1710
Qy      1561 TTTAGAACAGCATOCTATGATAATACAATTGCTTTCTCTACAAGTTGAGTCAAGGACAA 1620
Db      1711 TTTAGAACAGCATOCTATGATAATACAATTGCTTTCTCTACAAGTTGAGTCAAGGACAA 1770
Qy      1621 GGTGACTTGOCTOCTGAAAAAACT 1644
Db      1771 GGTGACTTGOCTOCTGAAAAAACT 1794

```

Title: US- 10- 615- 383A- 7
 Perfect score: 2976
 Sequence: 1 at at t gcaaaaaagact t at ccaacaaat at aaggt gt t g 2976

RESULT 4

US- 09- 134- 001C- 2477

; Sequence 2477, Application US/ 09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette- Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC- 007

; CURRENT APPLICATION NUMBER: US/ 09/ 134, 001C

; CURRENT FILING DATE: 1998- 08- 13

; PRIOR APPLICATION NUMBER: US 60/ 064, 964

PRI OR F I L I N G DATE: 1997-11-08
 PRI OR APPLI CATI ON NUMBER: US 60/055,779
 PRI OR F I L I N G DATE: 1997-08-14
 NUMBER OF SEQ I D NOS: 5674
 SEQ I D NO 2477
 LENGTH: 2793
 TYPE: DNA
 ORGANI SM St aphyl ococcus epi der mi di s
 US-09-134-001G-2477

Query Match 93.8% Score 2791.4; DB 3; Length 2793;
 Best Local Similarity 99.9%
 Matches 2792; Conservative 0; M smat ches 1; Indel s 0; Gaps 0;

Qy	102	TTAAAAAAAAATAATTTACTAACTAAAAAGAAAOCTATAGCAAATAAATCCAATAAATAT	161
Db	1	TTAAAAAAAAATAATTTACTAACTAAAAAGAAAOCTATAGCAAATAAATCCAATAAATAT	60
Qy	162	GCAATTAGAAAATTCACAGTAGGTACAGOGTCTATTGTAATAGGTGCAGCATTATTGTTT	221
Db	61	GCAATTAGAAAATTCACAGTAGGTACAGOGTCTATTGTAATAGGTGCAACATTATTGTTT	120
Qy	222	GGTTTAGGTCAATAATGAGGCCAAAGCTGAGGAGAATACAGTACAAGACGTTAAAGATTG	281
Db	121	GGTTTAGGTCAATAATGAGGCCAAAGCTGAGGAGAATACAGTACAAGACGTTAAAGATTG	180
Qy	282	AATATGGATGATGAATTATCAGATAGCAATGATCAGTCCAGTAATGAAGAAAAGAATGAT	341
Db	181	AATATGGATGATGAATTATCAGATAGCAATGATCAGTCCAGTAATGAAGAAAAGAATGAT	240
Qy	342	GTAATCAATAATAGTCAGTCAATAAACACCGATGATGATAACCAAATAAAAAAGAAGAA	401
Db	241	GTAATCAATAATAGTCAGTCAATAAACACCGATGATGATAACCAAATAAAAAAGAAGAA	300
Qy	402	ACGAATAGCAACGATGCCATAGAAAATCGCTCTAAAGATATAACACAGTCAACAACAAAT	461
Db	301	ACGAATAGCAACGATGCCATAGAAAATCGCTCTAAAGATATAACACAGTCAACAACAAAT	360
Qy	462	GTAGATGAAAACGAAGCAACATTTTTACAAAAGACCCCTCAAGATAATACTCAGCTTAAA	521
Db	361	GTAGATGAAAACGAAGCAACATTTTTACAAAAGACCCCTCAAGATAATACTCAGCTTAAA	420
Qy	522	GAAGAAGTGGTAAAAGAACCCCTCATCAGTCGAATCCTCAAATTCATCAATGGATACTGCC	581
Db	421	GAAGAAGTGGTAAAAGAACCCCTCATCAGTCGAATCCTCAAATTCATCAATGGATACTGCC	480
Qy	582	CAACAACCATCTCATACAACAATAAATAGTGAAGCATCTATTCAAACAAGTGATAATGAA	641
Db	481	CAACAACCATCTCATACAACAATAAATAGTGAAGCATCTATTCAAACAAGTGATAATGAA	540
Qy	642	GAAAATTCCCGGTATCAGATTTTGCTAACTCTAAAATAATAGAGAGTAACACTGAATCC	701
Db	541	GAAAATTCCCGGTATCAGATTTTGCTAACTCTAAAATAATAGAGAGTAACACTGAATCC	600
Qy	702	AATAAAGAAGAGAATACTATAGAGCAACCTAACAAAGTAAGAGAAGATTCAATAACAAGT	761
Db	601	AATAAAGAAGAGAATACTATAGAGCAACCTAACAAAGTAAGAGAAGATTCAATAACAAGT	660
Qy	762	CAACOGTCTAGCTATAAAAAATATAGATGAAAAAATTTCAAATCAAGATGAGTTATTAAAT	821
Db	661	CAACOGTCTAGCTATAAAAAATATAGATGAAAAAATTTCAAATCAAGATGAGTTATTAAAT	720
Qy	822	TTACCAATAAATGAATATGAAAATAAGGTTAGACGGTTATCTACAACATCTGCCAACCA	881

Db 721 TTACCAATAAATGAATATGAAAATAAGGTTAGACCGTTATCTACAACATCTGCCAAACCA 780
 Qy 882 TCGAGTAAGCGTGTAAACCGTAAATCAATTAGCGGCAGAACAAGGTTGAATGTTAATCAT 941
 Db 781 TCGAGTAAGCGTGTAAACCGTAAATCAATTAGCGGCAGAACAAGGTTGAATGTTAATCAT 840
 Qy 942 TTAATTAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGATGGTATTATT 1001
 Db 841 TTAATTAAGTTACTGATCAAAGTATTACTGAAGGATATGATGATAGTGATGGTATTATT 900
 Qy 1002 AAAGCACATGATGCTGAAAACCTTAATCTATGATGTAACCTTTGAAGTAGATGATAAGGTG 1061
 Db 901 AAAGCACATGATGCTGAAAACCTTAATCTATGATGTAACCTTTGAAGTAGATGATAAGGTG 960
 Qy 1062 AAATCTGGTGATACGATGACAGTGAATATAGATAAGAATACAGTTCATCAGATTTAAOC 1121
 Db 961 AAATCTGGTGATACGATGACAGTGAATATAGATAAGAATACAGTTCATCAGATTTAAOC 1020
 Qy 1122 GATAGTTTTGCAATACCAAAAAATAAAAGATAATTCTGGAGAAATCATCGCTACAGGTA 1181
 Db 1021 GATAGTTTTGCAATACCAAAAAATAAAAGATAATTCTGGAGAAATCATCGCTACAGGTA 1080
 Qy 1182 TATGACAACACAAATAAACAAATTACCTACACTTTTACAGATTATGTAGATAAATATGAA 1241
 Db 1081 TATGACAACACAAATAAACAAATTACCTACACTTTTACAGATTATGTAGATAAATATGAA 1140
 Qy 1242 AATATTAAGCGCACCTTAAATTAACATCATACATTGATAAATCAAAGGTTCCAAATAAT 1301
 Db 1141 AATATTAAGCGCACCTTAAATTAACATCATACATTGATAAATCAAAGGTTCCAAATAAT 1200
 Qy 1302 AACACTAAGTTAGATGTAGAATATAAGACGGCCCTTTATCAGTAAATAAAACAATTACG 1361
 Db 1201 AACACTAAGTTAGATGTAGAATATAAGACGGCCCTTTATCAGTAAATAAAACAATTACG 1260
 Qy 1362 GTTGAATATCAAAAACCTAACGAAAAATCGGACTGCTAACCTTCAAAGTATGTTACAAAC 1421
 Db 1261 GTTGAATATCAAAAACCTAACGAAAAATCGGACTGCTAACCTTCAAAGTATGTTACAAAC 1320
 Qy 1422 ATAGATACGAAAAACCATACAGTTGAGCAAAACGATTTATATTAAOCTCTTCGTTATTCA 1481
 Db 1321 ATAGATACGAAAAACCATACAGTTGAGCAAAACGATTTATATTAAOCTCTTCGTTATTCA 1380
 Qy 1482 GCCAAAGAAACAAATGTAATATTTAGGGAATGGCGATGAAGGTTCAACAATTATCGAC 1541
 Db 1381 GCCAAAGAAACAAATGTAATATTTAGGGAATGGCGATGAAGGTTCAACAATTATCGAC 1440
 Qy 1542 GATAGTACAATCATTAAAGTTTATAAGGTTGGAGATAATCAAAATTTACCAGATAGTAAC 1601
 Db 1441 GATAGTACAATCATTAAAGTTTATAAGGTTGGAGATAATCAAAATTTACCAGATAGTAAC 1500
 Qy 1602 AGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCAATTAGGA 1661
 Db 1501 AGAATTTATGATTACAGTGAATATGAAGATGTCACAAATGATGATTATGCCAATTAGGA 1560
 Qy 1662 AATAATAATGACGTGAATATTAATTTTGGTAATATAGATTCAOCATATATTATTAAGTT 1721
 Db 1561 AATAATAATGACGTGAATATTAATTTTGGTAATATAGATTCAOCATATATTATTAAGTT 1620
 Qy 1722 ATTAGTAAATATGACCTAATAAGGACGATTACACGACGATACAGCAAACCTGTGACAATG 1781
 Db 1621 ATTAGTAAATATGACCTAATAAGGACGATTACACGACGATACAGCAAACCTGTGACAATG 1680

Qy 1782 CAAACGACTATAAATGAGTATACTGGTGAGTTTAGAACAGCATOCTATGATAATACAATT 1841
 Db 1681 CAAACGACTATAAATGAGTATACTGGTGAGTTTAGAACAGCATOCTATGATAATACAATT 1740
 Qy 1842 GCTTTCTCTACAAGTT CAGGTCAAGGACAAGGTGACTTGOCTOCTGAAAAAAGTTATAAA 1901
 Db 1741 GCTTTCTCTACAAGTT CAGGTCAAGGACAAGGTGACTTGOCTOCTGAAAAAAGTTATAAA 1800
 Qy 1902 ATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATAAT 1961
 Db 1801 ATCGGAGATTACGTATGGGAAGATGTAGATAAAGATGGTATTCAAAATACAAATGATAAT 1860
 Qy 1962 GAAAAACCGCTTAGTAATGTATTGGTAACTTTGAOCTATCCTGATGGAACCTTCAAAATCA 2021
 Db 1861 GAAAAACCGCTTAGTAATGTATTGGTAACTTTGAOCTATCCTGATGGAACCTTCAAAATCA 1920
 Qy 2022 GTCAGAACAGATGAAGAGGGGAAATATCAATTTGATGGGTAAAAAACGGATTGACTTAT 2081
 Db 1921 GTCAGAACAGATGAAGAGGGGAAATATCAATTTGATGGGTAAAAAACGGATTGACTTAT 1980
 Qy 2082 AAAATTACATTGAAACACOGGAAGGATATACGCOGACGCTTAAACATT CAGGAACAAAT 2141
 Db 1981 AAAATTACATTGAAACACOGGAAGGATATACGCOGACGCTTAAACATT CAGGAACAAAT 2040
 Qy 2142 CCTGCACTAGACTCAGAAGGCAATTCTGTATGGGTAACTATTAAOAGACAAGACGATATG 2201
 Db 2041 CCTGCACTAGACTCAGAAGGCAATTCTGTATGGGTAACTATTAAOAGACAAGACGATATG 2100
 Qy 2202 ACTATTGATAGCGGATTTTATCAAACACCTAAATATAGCTTAGGGAAGTATGTATGGTAT 2261
 Db 2101 ACTATTGATAGCGGATTTTATCAAACACCTAAATATAGCTTAGGGAAGTATGTATGGTAT 2160
 Qy 2262 GACACTAATAAAGATGGTATTCAAGGTGATGATGAAAAAGGAATCTCTGGAGTAAAAGTG 2321
 Db 2161 GACACTAATAAAGATGGTATTCAAGGTGATGATGAAAAAGGAATCTCTGGAGTAAAAGTG 2220
 Qy 2322 ACGTTAAAAGATGAAAAACGGAAATATCATTAGTACAACAACAAGTATGAAAATGGAAAG 2381
 Db 2221 ACGTTAAAAGATGAAAAACGGAAATATCATTAGTACAACAACAAGTATGAAAATGGAAAG 2280
 Qy 2382 TATCAATTTGATAATTTAAATAGTGGTAATTATATTGTTCATTTTGATAAACCTTCAGGT 2441
 Db 2281 TATCAATTTGATAATTTAAATAGTGGTAATTATATTGTTCATTTTGATAAACCTTCAGGT 2340
 Qy 2442 ATGACTCAAACAACAACAGATTCTGGTGATGATGACGAACAGGATGCTGATGGGAAGAA 2501
 Db 2341 ATGACTCAAACAACAACAGATTCTGGTGATGATGACGAACAGGATGCTGATGGGAAGAA 2400
 Qy 2502 GTCCATGTAAACAATTACTGATCATGATGACTTTAGTATAGATAACGGATACTATGATGAC 2561
 Db 2401 GTCCATGTAAACAATTACTGATCATGATGACTTTAGTATAGATAACGGATACTATGATGAC 2460
 Qy 2562 GACTCAGATT CAGATAGTGATT CAGACTCAGATAGOGACGACTCAGACTCOGATAGOGAT 2621
 Db 2461 GACTCAGATT CAGATAGTGATT CAGACTCAGATAGOGACGACTCAGACTCOGATAGOGAT 2520
 Qy 2622 TCOGACTCAGACAGOGACTCAGATT COGATAGTGATT CAGATT CAGACAGTGACTCAGAC 2681
 Db 2521 TCOGACTCAGACAGOGACTCAGATT COGATAGTGATT CAGATT CAGACAGTGACTCAGAC 2580
 Qy 2682 TCAGATAGTGATT CAGATT CAGACAGOGATT COGACTCAGACAGTGACTCAGGATTAGAC 2741
 Db 2581 TCAGATAGTGATT CAGATT CAGACAGOGATT COGACTCAGACAGTGACTCAGGATTAGAC 2640

```

Qy      2742 AATAGCTCAGATAAGAATACAAAAGATAAATTACCGGATACAGGAGCTAATGAAGATCAT 2801
      |||
Db      2641 AATAGCTCAGATAAGAATACAAAAGATAAATTACCGGATACAGGAGCTAATGAAGATCAT 2700
      |||
Qy      2802 GATTCTAAAGGCACATTACTTGGAGCTTTATTTGCAGGTTTAGGAGCGTTATTATTAGGG 2861
      |||
Db      2701 GATTCTAAAGGCACATTACTTGGAGCTTTATTTGCAGGTTTAGGAGCGTTATTATTAGGG 2760
      |||
Qy      2862 AAGCGTCGCAAAAATAGAAAAAATAAAAATTAA 2894
      |||
Db      2761 AAGCGTCGCAAAAATAGAAAAAATAAAAATTAA 2793
      |||

```

Title: US- 10- 615- 383A- 10
 Perfect score: 4824
 Sequence: 1 LKKNLLTKKKPI ANKSNKY. FAGLGALLLGKRRKNRKNKN 930

RESULT 3
 ABP40469

ID ABP40469 standard; protein; 930 AA.

XX

AC ABP40469;

XX

DT 24- JUL- 2002 (first entry)

XX

DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO: 5314.

XX

KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW antibacterial; gene therapy.

XX

OS Staphylococcus epidermidis.

XX

PN US6380370- B1.

XX

PD 30- APR- 2002.

XX

PF 13- AUG- 1998; 98US- 00134001.

XX

PR 14- AUG- 1997; 97US- 0055779P.

PR

08- NOV- 1997; 97US- 0064964P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Doucette- Stamm LA, Bush D;

XX

DR WPI; 2002- 381255/ 41.

DR

N- PSDB; ABN93014.

XX

PT Novel isolated nucleic acid encoding a Staphylococcus epidermis

PT

polypeptide, useful for diagnosing and treating bacterial infections.

XX

PS Disclosure; SEQ ID NO 5314; 267pp; English.

XX

CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life cycle
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from the USPTO web site

XX

SQ Sequence 930 AA;

Query Match 99.9% Score 4820; DB 1; Length 930;
 Best Local Similarity 99.9%
 Matches 929; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1 LKKNLLT KKKPI ANKSNKYAI RKFTVGTASI VI GAALLFGLGHNEAKAEENTVQDVKDS 60
Db      1 LKKNLLT KKKPI ANKSNKYAI RKFTVGTASI VI GATLLFGLGHNEAKAEENTVQDVKDS 60

Qy     61 NMDELSDSNDQSSNEEKNDVI NNSQSI NTDDDNQI KKEETNSNDI ENRSKDI TQSTTN 120
Db     61 NMDELSDSNDQSSNEEKNDVI NNSQSI NTDDDNQI KKEETNSNDI ENRSKDI TQSTTN 120

Qy    121 VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTI NSEASI QTSDNE 180
Db    121 VDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTI NSEASI QTSDNE 180

Qy    181 ENSRVSDFANSKI | ESNTESNKEENTI EQPNKVREDSI TSQPSSYKNI DEKI SNQDELLN 240
Db    181 ENSRVSDFANSKI | ESNTESNKEENTI EQPNKVREDSI TSQPSSYKNI DEKI SNQDELLN 240

Qy    241 LPI NEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLI KVTDQSI TEGYDDSDGI | 300
Db    241 LPI NEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLI KVTDQSI TEGYDDSDGI | 300

Qy    301 KAHDAENLI YDVTFEVDDKVKSGDTMTVNI DKNTVPSDLTDSFAI PKI KDNSGEI | ATGT 360
Db    301 KAHDAENLI YDVTFEVDDKVKSGDTMTVNI DKNTVPSDLTDSFAI PKI KDNSGEI | ATGT 360

Qy    361 YDNTNKQI TYTFTDYVDKYENI KAHLKLTYSI DSKVPNNNTKLDVEYKTALSSVNKTI T 420
Db    361 YDNTNKQI TYTFTDYVDKYENI KAHLKLTYSI DSKVPNNNTKLDVEYKTALSSVNKTI T 420

Qy    421 VEYQKPENRTANLQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVNI SGNGDEGSTI | D 480
Db    421 VEYQKPENRTANLQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVNI SGNGDEGSTI | D 480

Qy    481 DSTI | KVKVGDNQNL PDSNRI YDYSEYEDVTNDDYAQLGNNDVNI NFGNI DSPYI | KV 540
Db    481 DSTI | KVKVGDNQNL PDSNRI YDYSEYEDVTNDDYAQLGNNDVNI NFGNI DSPYI | KV 540

Qy    541 | SKYDPNKDDYTTI QQTVTMQTTI NEYTGEFRTASYDNTI AFSTSSGQGGDLPEKTYK 600
Db    541 | SKYDPNKDDYTTI QQTVTMQTTI NEYTGEFRTASYDNTI AFSTSSGQGGDLPEKTYK 600

Qy    601 | GDYWMEDVDKDG I QNTNDNEKPLSNVL VTLTPDGTSKSVRTDEEGKYQFDGLKNGLTY 660
Db    601 | GDYWMEDVDKDG I QNTNDNEKPLSNVL VTLTPDGTSKSVRTDEEGKYQFDGLKNGLTY 660

Qy    661 K I TFETPEGYTPTLKHSGTNPALDSEGNSVWWTI NGQDDMTI DSGFYQTPKYSLGNYVWV 720
Db    661 K I TFETPEGYTPTLKHSGTNPALDSEGNSVWWTI NGQDDMTI DSGFYQTPKYSLGNYVWV 720

Qy    721 DTNKDGI QGDDEKGI SGVKVTLKDENGNI | STTTT DENGKYQFDNLNSGNYI VHFDPKPSG 780
Db    721 DTNKDGI QGDDEKGI SGVKVTLKDENGNI | STTTT DENGKYQFDNLNSGNYI VHFDPKPSG 780

Qy    781 MTQTTTTDSGDDDEQDADGEEVHVTI TDHDDFSI DNGYYDDSDSDSDSDSDSDSDSDSDSDSDSDSDSD 840
Db    781 MTQTTTTDSGDDDEQDADGEEVHVTI TDHDDFSI DNGYYDDSDSDSDSDSDSDSDSDSDSDSDSDSDSD 840

```


Qy 841 SDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSL DNSSDKNTKDKLPDTGANEDH 900
 Db 841 SDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSDSL DNSSDKNTKDKLPDTGANEDH 900
 Qy 901 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 930
 Db 901 DSKGTLLGALFAGLGALLLGKRRKNRKNKN 930

Title: US- 10- 615- 383A- 10_COPY_51_598
 Perfect score: 2808
 Sequence: 1 ENTVDVKDSNMDELSDSN. TI AFSTSSGQGGDLPEKT 548

RESULT 4

ABP40469

ID ABP40469 standard; protein; 930 AA.

XX

AC ABP40469;

XX

DT 24- JUL- 2002 (first entry)

XX

DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO: 5314.

XX

KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
 KW antibacterial; gene therapy.

XX

OS Staphylococcus epidermidis.

XX

PN US6380370- B1.

XX

PD 30- APR- 2002.

XX

PF 13- AUG- 1998; 98US- 00134001.

XX

PR 14- AUG- 1997; 97US- 0055779P.

PR

08- NOV- 1997; 97US- 0064964P.

XX

PA (GENO-) GENOME THERAPEUTICS CORP.

XX

PI Doucette- Stamm LA, Bush D;

XX

DR WPI; 2002- 381255/ 41.

DR

N- PSDB; ABN93014.

XX

PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
 PT polypeptide, useful for diagnosing and treating bacterial infections.

XX

PS Disclosure; SEQ ID NO 5314; 267pp; English.

XX

CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life cycle
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site

XX

SQ Sequence 930 AA;

Query Match 100.0% Score 2808; DB 1; Length 930;
 Best Local Similarity 100.0%
 Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1  ENTVDVKDSNMDELSDSNDQSSNEEKNDVI NNSQSI NTDDDNQI KKEETNSNDI ENR 60
Db      51  ENTVDVKDSNMDELSDSNDQSSNEEKNDVI NNSQSI NTDDDNQI KKEETNSNDI ENR 110
Qy     61  SKDI TQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTI NS 120
Db    111  SKDI TQSTTNVDENEATFLQKTPQDNTQLKEEVVKEPSSVESSNSSMDTAQQPSHTTI NS 170
Qy    121  EASI QTSDNEENSRVSDFANSKI | ESNTESNKEENTI EQPNKVREDSI TSQPSSYKNI DE 180
Db    171  EASI QTSDNEENSRVSDFANSKI | ESNTESNKEENTI EQPNKVREDSI TSQPSSYKNI DE 230
Qy    181  KI SNQDELLNLPI NEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLI KVTDQSI T 240
Db    231  KI SNQDELLNLPI NEYENKVRPLSTTSAQPSSKRVTVNQLAAEQGSNVNHLI KVTDQSI T 290
Qy    241  EGYDDSDGI | KAHDAENLI YDVTFEVDDKVKSGDTMTVNI DKNTVPSDLTDSFAI PKI KD 300
Db    291  EGYDDSDGI | KAHDAENLI YDVTFEVDDKVKSGDTMTVNI DKNTVPSDLTDSFAI PKI KD 350
Qy    301  NSGEI | ATGTYDNTNKQI TYTFTDYVDKYENI KAHLKLTSYI DSKVPNNNTKLDVEYKT 360
Db    351  NSGEI | ATGTYDNTNKQI TYTFTDYVDKYENI KAHLKLTSYI DSKVPNNNTKLDVEYKT 410
Qy    361  ALSSVNKTI TVEYQKPNENRTANLQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVNI SG 420
Db    411  ALSSVNKTI TVEYQKPNENRTANLQSMFTNI DTKNHTVEQTI YI NPLRYSAKETNVNI SG 470
Qy    421  NGDEGSTI | DDSTI | KVKYKVDNQNL PDSNRI YDYSEYEDVTNDDYAQLGNNDVNI NFG 480
Db    471  NGDEGSTI | DDSTI | KVKYKVDNQNL PDSNRI YDYSEYEDVTNDDYAQLGNNDVNI NFG 530
Qy    481  NI DSPYI | KVI SKYDPNKDDYTTI QQTVTMQTTI NEYTGEFRTASYDNTI AFSTSSGQQQ 540
Db    531  NI DSPYI | KVI SKYDPNKDDYTTI QQTVTMQTTI NEYTGEFRTASYDNTI AFSTSSGQQQ 590
Qy    541  GDLPEKT 548
Db    591  GDLPEKT 598

```